CLAIMS

1. A method for identifying inhibitor compounds capable of reducing the interaction between:

a) a first region which is a signature motif on a nuclear protein, and

b) a second region which is that part of a nuclear receptor which is capable of interacting with the nuclear protein through binding to the signature motif,

wherein:

the nuclear protein is a bridging factor that is responsible for the interaction between a liganded nuclear receptor and a transcription initiation complex involved in regulation of gene expression;

the nuclear receptor is a transcription factor;

the signature motif is a short sequence of amino acid residues which is the key structural element of a nuclear protein which binds to a liganded nuclear receptor as part of the process of the activation or repression of target genes; and

in which the method comprises taking:

i) the potential inhibitor compound;

ii) the liganded nuclear receptor or a fragment thereof in which the fragment comprises the second region defined in this claim in b) above;

iii) a fragment comprising a signature motif of the nuclear protein; and

iv) detecting the presence or absence of inhibition of the interaction between ii) and iii).

2 A method according to claim 1 in which the signature motif is B^1XXLL in which B^1 is any natural hydrophobic amino acid, L is leucine and X independently represents any natural amino acid.

3 A method according to claim 2 in which B^1 is leucine or valine.

4 A method according to claim 3 in which B^1 is leucine.

5 A method according to any one of claims 2-4 in which the signature motif is further defined as B^2B^1XXLL wherein B^2 is a hydrophobic amino acid.

6 A method according to claim 5 in which B^2 is selected from the group consisting of isoleucine, leucine, methionine, phenylalanine, tryptophan, tyrosine and valine.

7. A method according to any one of claims 1-6 in which the nuclear protein is a coactivator.

8. A method according to claim 7 in which the coactivator is selected from the group consisting of RIP 140, SRC-1, TIF2, CBP, p300, TIF1, Trip1, Trip2, Trip3, Trip4, Trip5, Trip8, Trip9, p/CIP, ARA70 & Trip230.

9. A method according to any one of claims 1-6 in which the transcription factor is a steroid hormone receptor.

10. A method according to claim 9 in which the steroid hormone receptor is selected from the group consisting of oestrogen receptor, progesterone receptor, androgen receptor and glucocorticoid receptor.

11. A method according to claim 10 in which the steroid hormone receptor is oestrogen receptor.

12. A method according to any preceding claim wherein the method is in the form of a 2-hybrid assay system.

13 A method according to any preceding claim wherein the potential inhibitor is in the form of a peptide library based on a signature motif as defined in any one of claims 2-6.

14. A novel inhibitor identified according to the method defined in any one of claims 1-13 which reduces the interaction between

a) a first region which is a signature motif on a nuclear protein, and

b) a second region which is that part of a nuclear receptor which is capable of interacting with the nuclear protein through binding to the signature motif,

wherein:

the nuclear protein is a bridging factor that is responsible for the interaction between a liganded nuclear receptor and the transcription initiation complex involved in regulation of gene expression;

the nuclear receptor is a transcription factor;

the signature motif is a short sequence of amino acid residues which is the key structural element of a nuclear protein which binds to a liganded nuclear receptor as part of the process of the activation or repression of target genes.

15 An inhibitor according to claim 14 which is a peptide of less than 15 amino acid residues comprising the signature motif defined in any one of claims 1-6.

16 An inhibitor according to claim 15 selected from the group consisting of PQAQQKSLLQQLLT (SEQ ID NO: 2), KLVQLLTTT (SEQ ID NO: 3), ILHRLLQE (SEQ ID NO: 4) and LLQQLLTE (SEQ ID NO: 5).

17 An inhibitor according to claim 14 comprising an antibody which specifically binds to a signature motif on a nuclear protein.

18 A pharmaceutical composition which comprises an inhibitor as defined in any one of claims 14-17 or a pharmaceutically-acceptable salt thereof, in association with a pharmaceutically-acceptable diluent or carrier.

19 A method of mapping nuclear receptor interaction domains in nuclear proteins in which the method comprises analysis of the sequence of a nuclear protein for the presence of signature motifs as defined in any one of claims 1-6 in order to identify an interaction domain or a potential interaction domain.